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APPLICANT
DAHIYAT et al.

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OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)		
THW	7	Bowie et al., "A Method to Identify Protein Sequences that Fold into a Known Three-Dimensional Structure," <i>Science</i> 253:164-170 (1991)
↓	8	Dahiyat and Mayo, "Protein Design automation", <i>Protein Science</i> 5:895-903 (1996)
↓	9	Dahiyat and Mayo, "De Novo Protein Design: Fully Automated Sequence Selection," <i>Science</i> 278:82-87 (1997)

EXAMINER

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EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not considered.

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10	Desjarlais and Handel, "De novo design of the hydrophobic cores of proteins", <i>Protein Science</i> 4:2006-2018 (1995)
11	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils", <i>Proc. Natl. Acad. Sci. USA</i> 92:8408-8412 (1995)
12	Kono and Doi, "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction From Given Backbone Geometry", <i>Proteins: Structure, Function and Genetics</i> 19:244-255 (1994)
13	Hellinga, et al., "Optimal sequence selection in proteins of known structure by simulated evolution", <i>Proc. Natl. Acad. Sci., USA</i> Vol.91:5803-5807 (1994)
14	Jones, "De novo protein design using pairwise potentials and a genetic algorithm", <i>Protein Science</i> 3:567-574 (1994)
15	Lam et al., "Application of combinatorial library methods in cancer research and drug discovery," <i>Anti-Cancer Drug Design</i> 12:145-167 (1997)
16	Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery. 1. Background and Peptide Combinatorial Libraries," <i>J Med Chem</i> 37(9):1233-1251 (Apr 1994)